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<110> Presnell, Scott R.
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<120> CYTOKINE RECEPTOR ZCYTOR19

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<150> US 60/253,561
<151> 2000-11-28

<150> US 60/267,211
<151> 2001-02-07

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<170> FastSEQ for Windows Version 3.0

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<211> 1476
<212> DNA
<213> Homo sapiens

<220>
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Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
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gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg      96
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
      20              25              30

ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc      144

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Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly	
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Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr	
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cgt	aga	cgg	tgg	cgc	gaa	gtg	gaa	gag	tgt	gcg	gga	acc	aag	gag	ctg	240
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu	
65					70				75					80		
cta	tgt	tct	atg	atg	tgc	ctg	aag	aaa	cag	gac	ctg	tac	aac	aag	ttc	288
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe	
			85					90					95			
aag	gga	cgc	gtg	cgg	acg	gtt	tct	ccc	agc	tcc	aag	tcc	ccc	tgg	gtg	336
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val	
		100					105					110				
gag	tcc	gaa	tac	ctg	gat	tac	ctt	ttt	gaa	gtg	gag	ccg	gcc	cca	cct	384
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro	
	115					120					125					
gtc	ctg	gtg	ctc	acc	cag	acg	gag	gag	atc	ctg	agt	gcc	aat	gcc	acg	432
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr	
	130				135				140							
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Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Phe	Leu	Lys	Tyr	Glu	Val	
145					150				155					160		
gca	ttt	tgg	ggg	ggg	ggg	gcc	gga	acc	aag	acc	cta	ttt	cca	gtc	act	528
Ala	Phe	Trp	Gly	Gly	Gly	Ala	Gly	Thr	Lys	Thr	Leu	Phe	Pro	Val	Thr	
			165					170					175			
ccc	cat	ggc	cag	cca	gtc	cag	atc	act	ctc	cag	cca	gct	gcc	agc	gaa	576
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu	
		180					185					190				
cac	cac	tgc	ctc	agt	gcc	aga	acc	atc	tac	acg	ttc	agt	gtc	ccg	aaa	624
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys	
	195						200				205					

[illegible]

caa ggg ccg ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa 1200
 Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu
 385 390 395 400

ttc tcc aag gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc 1248
 Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu
 405 410 415

tcc tcc tgg gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc 1296
 Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val
 420 425 430

cct ggg gga ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa 1344
 Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu
 435 440 445

agc agc cct gag gag gaa gag gag gcg agg gaa tca gaa att gag gac 1392
 Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp
 450 455 460

agc gat gcg ggc agc tgg ggg gct gag agc acc cag agg acc gag gac 1440
 Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp
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agg ggc cgg aca ttg ggg cat tac atg gcc agg tga 1476
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<210> 2

<211> 491

<212> PRT

<213> Homo sapiens

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 20 25 30
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45

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Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe
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Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val
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Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro
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Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr
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Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Phe	Leu	Lys	Tyr	Glu	Val
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Ala	Phe	Trp	Gly	Gly	Gly	Ala	Gly	Thr	Lys	Thr	Leu	Phe	Pro	Val	Thr
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Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu
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His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys
	195					200					205				
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu
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Ala	Asn	Trp	Ala	Phe	Leu	Val	Leu	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu
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Val	Ile	Ala	Ala	Gly	Gly	Val	Ile	Trp	Lys	Thr	Leu	Met	Gly	Asn	Pro
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Trp	Phe	Gln	Arg	Ala	Lys	Met	Pro	Arg	Ala	Leu	Glu	Leu	Thr	Arg	Gly
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Val	Arg	Pro	Thr	Pro	Arg	Val	Arg	Ala	Pro	Ala	Thr	Gln	Gln	Thr	Arg
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Trp	Lys	Lys	Asp	Leu	Ala	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Asp
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Thr	Glu	Asp	Gly	Val	Ser	Phe	Gln	Pro	Tyr	Ile	Glu	Pro	Pro	Ser	Phe
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Leu	Gly	Gln	Glu	His	Gln	Ala	Pro	Gly	His	Ser	Glu	Ala	Gly	Gly	Val
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Asp	Ser	Gly	Arg	Pro	Arg	Ala	Pro	Leu	Val	Pro	Ser	Glu	Gly	Ser	Ser
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Ala	Trp	Asp	Ser	Ser	Asp	Arg	Ser	Trp	Ala	Ser	Thr	Val	Asp	Ser	Ser
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Trp	Asp	Arg	Ala	Gly	Ser	Ser	Gly	Tyr	Leu	Ala	Glu	Lys	Gly	Pro	Gly
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Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu
 385 390 395 400
 Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu
 405 410 415
 Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val
 420 425 430
 Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu
 435 440 445
 Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp
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<212> DNA

<213> Artificial Sequence

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<223> n = A,T,C or G

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ytnacntggy tncnnggnyt nggnaayccn cargaygt na cntayttygt ngcntaycar	180
wsnwsnccna cnmgmngmng ntggmngar gtngargart gygcnggnac naargarytn	240
ytnygywsna tgatgtgyt naaraarcar gayytnaya ayaarttyaa rggmngntn	300
mgnacngtnw snccnwsnws naarwsnccn tgggtngarw sngartayyt ngaytaytn	360
ttygargtng arcngcncc nccngtnytn gtnytnacn aracngarga rathytnwsn	420
gcnaaygcna cntaycaryt nccncntgy atgccnccny tnttytnaa rtaygargtn	480
gcnttytggg gngngngngc nggnacnaar acnytnntyc cngtnacncc ncayggncar	540
ccngtnccara thacnytnca rccngcngcn wsngarcayc aytgyytnws ngcnmgna	600
athtayacnt tywsngtncc naartaywsn aarttywsna arccnacntg yttyytnytn	660
gargtnccng argcnaaytg ggcnttyytn gtnytnccnw snytnytnat hytnytnytn	720
gtathgcng cngngngngt nathtggaar acnytnatgg gnaayccntg gttycarmgn	780
gcnaaratgc cnmgngcnytn ngarytnacn mgngngntnm gncnacncc nmngntnmgn	840
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<213> Homo sapiens
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Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr	Arg	Arg	Arg	Trp
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Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu	Leu	Cys	Ser	Met
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Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe	Lys	Gly	Arg	Val
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Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val	Glu	Ser	Glu	Tyr
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Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro	Val	Leu	Val	Leu
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Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr	Tyr	Gln	Leu	Pro
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Pro	Cys	Met	Pro	Pro	Leu	Phe	Leu	Lys	Tyr	Glu	Val	Ala	Phe	Trp	Gly
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Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu	His	His	Cys	Leu
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Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys	Tyr	Ser	Lys	Phe
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<222> (1)...(5)
<223> Xaa = Any Amino Acid
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<223> Oligonucleotide primer ZC21195

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<210> 8
<211> 25
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<223> Oligonucleotide primer ZC14063

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<211> 21

<213> Artificial Sequence

<223> Oligonucleotide primer ZC17574

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21

<211> 24

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<223> Oligonucleotide primer ZC17600

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24

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<213> Artificial Sequence

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Glu Tyr Met Pro Met Glu

5

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG peptide tag

<400> 12

Asp Tyr Lys Asp Asp Asp Lys

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<210> 13

<211> 699

<212> DNA

<213> Homo sapiens

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acccttgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	180
aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	240
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggttgaat	300
ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	catcctccat	cgagaaaacc	360
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aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	660
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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(990)

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agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	96	
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr		
			20					25					30				
ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	144	
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser		
			35					40					45				
ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	192	
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser		
			50					55					60				
ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	240	
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr		
65						70					75					80	
tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	288	
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys		
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aaa	gtt	gag	ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	336	
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys		
			100					105					110				
cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	384	
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro		
			115					120					125				
aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	432	
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys		
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gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	480	
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp		
145						150					155			160			
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Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu		
			165					170						175			
gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	576	
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu		
			180					185					190				

cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac 624
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205

aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg 672
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220

cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag 720
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 225 230 235 240

ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat 768
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255

ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac 816
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270

aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc 864
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285

ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac 912
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300

gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg 960
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320

cag aag agc ctc tcc ctg tct ccg ggt aaa 990
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 15

<211> 330

<212> PRT

<213> Homo sapiens

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Phe	Pro	Glu 35	Pro	Val	Thr	Val	Ser 40	Trp	Asn	Ser	Gly	Ala 45	Leu	Thr	Ser
Gly 50	Val	His	Thr	Phe	Pro	Ala 55	Val	Leu	Gln	Ser	Ser 60	Gly	Leu	Tyr	Ser
Leu 65	Ser	Ser	Val	Val	Thr 70	Val	Pro	Ser	Ser	Ser 75	Leu	Gly	Thr	Gln	Thr 80
Tyr	Ile	Cys	Asn 85	Val	Asn	His	Lys	Pro	Ser 90	Asn	Thr	Lys	Val 95	Asp	Lys
Lys	Val	Glu 100	Pro	Lys	Ser	Cys	Asp 105	Lys	Thr	His	Thr	Cys 110	Pro	Pro	Cys
Pro	Ala 115	Pro	Glu	Leu	Leu	Gly	Gly 120	Pro	Ser	Val	Phe	Leu 125	Phe	Pro	Pro
Lys 130	Pro	Lys	Asp	Thr	Leu	Met 135	Ile	Ser	Arg	Thr	Pro 140	Glu	Val	Thr	Cys
Val 145	Val	Val	Asp	Val	Ser 150	His	Glu	Asp	Pro	Glu	Val 155	Lys	Phe	Asn	Trp 160
Tyr	Val	Asp	Gly 165	Val	Glu	Val	His	Asn	Ala 170	Lys	Thr	Lys	Pro 175	Arg	Glu
Glu	Gln	Tyr	Asn 180	Ser	Thr	Tyr	Arg	Val 185	Val	Ser	Val	Leu 190	Thr	Val	Leu
His 195	Gln	Asp	Trp	Leu	Asn	Gly 200	Lys	Glu	Tyr	Lys	Cys 205	Lys	Val	Ser	Asn
Lys 210	Ala	Leu	Pro	Ala	Pro	Ile 215	Glu	Lys	Thr	Ile	Ser 220	Lys	Ala	Lys	Gly
Gln 225	Pro	Arg	Glu	Pro	Gln 230	Val	Tyr	Thr	Leu	Pro	Pro 235	Ser	Arg	Asp	Glu 240
Leu	Thr	Lys	Asn 245	Gln	Val	Ser	Leu	Thr	Cys 250	Leu	Val	Lys	Gly	Phe	Tyr 255
Pro	Ser	Asp	Ile 260	Ala	Val	Glu	Trp	Glu 265	Ser	Asn	Gly	Gln 270	Pro	Glu	Asn
Asn	Tyr	Lys 275	Thr	Thr	Pro	Pro	Val	Leu 280	Asp	Ser	Asp	Gly 285	Ser	Phe	Phe
Leu 290	Tyr	Ser	Lys	Leu	Thr	Val 295	Asp	Lys	Ser	Arg	Trp 300	Gln	Gln	Gly	Asn
Val 305	Phe	Ser	Cys	Ser	Val 310	Met	His	Glu	Ala	Leu 315	His	Asn	His	Tyr	Thr 320
Gln	Lys	Ser	Leu 325	Ser	Leu	Ser	Pro	Gly 330	Lys						

<210> 16
 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(321)

<400> 16

act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag	48
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln	
1 5 10 15	
ttg aaa tct ggt acc gcc tct gtt gtg tgc ctg ctg aat aac ttc tat	96
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr	
20 25 30	
ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg	144
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser	
35 40 45	
ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc	192
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr	
50 55 60	
tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa	240
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys	
65 70 75 80	
cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc	288
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro	
85 90 95	
gtc aca aag agc ttc aac agg gga gag tgt tag	321
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *	
100 105	

<210> 17
 <211> 106
 <212> PRT

<213> Homo sapiens

<400> 17

Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln
1				5				10					15		
Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr
			20					25					30		
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser
		35					40					45			
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr
	50					55				60					
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys
65					70					75				80	
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro
				85				90						95	
Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys						
			100					105							

<210> 18

<211> 1563

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1563)

<400> 18

atg	gcg	ggg	ccc	gag	cgc	tgg	ggc	ccc	ctg	ctc	ctg	tgc	ctg	ctg	cag	48
Met	Ala	Gly	Pro	Glu	Arg	Trp	Gly	Pro	Leu	Leu	Leu	Cys	Leu	Leu	Gln	
1				5				10						15		
gcc	gct	cca	ggg	agg	ccc	cgt	ctg	gcc	cct	ccc	cag	aat	gtg	acg	ctg	96
Ala	Ala	Pro	Gly	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu	
			20					25					30			
ctc	tcc	cag	aac	ttc	agc	gtg	tac	ctg	aca	tgg	ctc	cca	ggg	ctt	ggc	144
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly	
			35				40					45				
aac	ccc	cag	gat	gtg	acc	tat	ttt	gtg	gcc	tat	cag	agc	tct	ccc	acc	192
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr	
			50				55				60					

cgt	aga	cgg	tgg	cgc	gaa	gtg	gaa	gag	tgt	gcg	gga	acc	aag	gag	ctg	240
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu	
65					70					75					80	
cta	tgt	tct	atg	atg	tgc	ctg	aag	aaa	cag	gac	ctg	tac	aac	aag	ttc	288
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe	
				85					90						95	
aag	gga	cgc	gtg	cgg	acg	gtt	tct	ccc	agc	tcc	aag	tcc	ccc	tgg	gtg	336
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val	
			100					105					110			
gag	tcc	gaa	tac	ctg	gat	tac	ctt	ttt	gaa	gtg	gag	ccg	gcc	cca	cct	384
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro	
		115					120					125				
gtc	ctg	gtg	ctc	acc	cag	acg	gag	gag	atc	ctg	agt	gcc	aat	gcc	acg	432
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr	
	130					135					140					
tac	cag	ctg	ccc	ccc	tgc	atg	ccc	cca	ctg	gat	ctg	aag	tat	gag	gtg	480
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val	
145					150					155					160	
gca	ttc	tgg	aag	gag	ggg	gcc	gga	aac	aag	acc	cta	ttt	cca	gtc	act	528
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr	
			165					170						175		
ccc	cat	ggc	cag	cca	gtc	cag	atc	act	ctc	cag	cca	gct	gcc	agc	gaa	576
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu	
			180					185					190			
cac	cac	tgc	ctc	agt	gcc	aga	acc	atc	tac	acg	ttc	agt	gtc	ccg	aaa	624
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys	
		195					200					205				
tac	agc	aag	ttc	tct	aag	ccc	acc	tgc	ttc	ttg	ctg	gag	gtc	cca	gaa	672
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu	
	210					215					220					
gcc	aac	tgg	gct	ttc	ctg	gtg	ctg	cca	tcg	ctt	ctg	ata	ctg	ctg	tta	720

Ala	Asn	Trp	Ala	Phe	Leu	Val	Leu	Pro	Ser	Leu	Ile	Leu	Leu	Leu	
225					230					235				240	
gta	att	gcc	gca	ggg	ggg	gtg	atc	tgg	aag	acc	ctc	atg	ggg	aac	ccc
Val	Ile	Ala	Ala	Gly	Gly	Val	Ile	Trp	Lys	Thr	Leu	Met	Gly	Asn	Pro
				245					250					255	
tgg	ttt	cag	cgg	gca	aag	atg	cca	cgg	gcc	ctg	gac	ttt	tct	gga	cac
Trp	Phe	Gln	Arg	Ala	Lys	Met	Pro	Arg	Ala	Leu	Asp	Phe	Ser	Gly	His
			260					265					270		
aca	cac	cct	gtg	gca	acc	ttt	cag	ccc	agc	aga	cca	gag	tcc	gtg	aat
Thr	His	Pro	Val	Ala	Thr	Phe	Gln	Pro	Ser	Arg	Pro	Glu	Ser	Val	Asn
		275					280					285			
gac	ttg	ttc	ctc	tgt	ccc	caa	aag	gaa	ctg	acc	aga	ggg	gtc	agg	ccg
Asp	Leu	Phe	Leu	Cys	Pro	Gln	Lys	Glu	Leu	Thr	Arg	Gly	Val	Arg	Pro
	290					295					300				
acg	cct	cga	gtc	agg	gcc	cca	gcc	acc	caa	cag	aca	aga	tgg	aag	aag
Thr	Pro	Arg	Val	Arg	Ala	Pro	Ala	Thr	Gln	Gln	Thr	Arg	Trp	Lys	Lys
305					310					315					320
gac	ctt	gca	gag	gac	gaa	gag	gag	gag	gat	gag	gag	gac	aca	gaa	gat
Asp	Leu	Ala	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Asp	Thr	Glu	Asp
				325					330					335	
ggc	gtc	agc	ttc	cag	ccc	tac	att	gaa	cca	cct	tct	ttc	ctg	ggg	caa
Gly	Val	Ser	Phe	Gln	Pro	Tyr	Ile	Glu	Pro	Pro	Ser	Phe	Leu	Gly	Gln
			340					345					350		
gag	cac	cag	gct	cca	ggg	cac	tcg	gag	gct	ggg	ggg	gtg	gac	tca	ggg
Glu	His	Gln	Ala	Pro	Gly	His	Ser	Glu	Ala	Gly	Gly	Val	Asp	Ser	Gly
		355					360					365			
agg	ccc	agg	gct	cct	ctg	gtc	cca	agc	gaa	ggc	tcc	tct	gct	tgg	gat
Arg	Pro	Arg	Ala	Pro	Leu	Val	Pro	Ser	Glu	Gly	Ser	Ser	Ala	Trp	Asp
	370					375					380				
tct	tca	gac	aga	agc	tgg	gcc	agc	act	gtg	gac	tcc	tcc	tgg	gac	agg
Ser	Ser	Asp	Arg	Ser	Trp	Ala	Ser	Thr	Val	Asp	Ser	Ser	Trp	Asp	Arg
385					390					395					400

gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc caa ggg ccg 1248
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro
 405 410 415

ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa ttc tcc aag 1296
 Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys
 420 425 430

gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc tcc tcc tgg 1344
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp
 435 440 445

gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc cct ggg gga 1392
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly
 450 455 460

ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa agc agc cct 1440
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
 465 470 475 480

gag gag gaa gag gag gcg agg gaa tca gaa att gag gac agc gat gcg 1488
 Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
 485 490 495

ggc agc tgg ggg gct gag agc acc cag agg acc gag gac agg ggc cgg 1536
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg
 500 505 510

aca ttg ggg cat tac atg gcc agg tga 1563
 Thr Leu Gly His Tyr Met Ala Arg *

 515 520

<210> 19

<211> 520

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1 5 10 15
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30

Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
 165 170 175
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
 180 185 190
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
 195 200 205
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
 210 215 220
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu
 225 230 235 240
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
 245 250 255
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His
 260 265 270
 Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn
 275 280 285
 Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro
 290 295 300
 Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys
 305 310 315 320
 Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp
 325 330 335
 Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln
 340 345 350
 Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly
 355 360 365

0099558-11201

Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp
 370 375 380
 Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg
 385 390 395 400
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro
 405 410 415
 Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys
 420 425 430
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp
 435 440 445
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly
 450 455 460
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
 465 470 475 480
 Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
 485 490 495
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg
 500 505 510
 Thr Leu Gly His Tyr Met Ala Arg
 515 520

<210> 20

<211> 674

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(633)

<400> 20

atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg ctg cag	48
Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln	
1 5 10 15	
gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg	96
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu	
20 25 30	
ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc	144
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly	
35 40 45	

aac	ccc	cag	gat	gtg	acc	tat	ttt	gtg	gcc	tat	cag	agc	tct	ccc	acc	192
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr	
50						55				60						
cgt	aga	cgg	tgg	cgc	gaa	gtg	gaa	gag	tgt	gcg	gga	acc	aag	gag	ctg	240
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu	
65						70				75				80		
cta	tgt	tct	atg	atg	tgc	ctg	aag	aaa	cag	gac	ctg	tac	aac	aag	ttc	288
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe	
				85				90						95		
aag	gga	cgc	gtg	cgg	acg	gtt	tct	ccc	agc	tcc	aag	tcc	ccc	tgg	gtg	336
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val	
		100						105				110				
gag	tcc	gaa	tac	ctg	gat	tac	ctt	ttt	gaa	gtg	gag	ccg	gcc	cca	cct	384
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro	
		115				120						125				
gtc	ctg	gtg	ctc	acc	cag	acg	gag	gag	atc	ctg	agt	gcc	aat	gcc	acg	432
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr	
130						135				140						
tac	cag	ctg	ccc	ccc	tgc	atg	ccc	cca	ctg	gat	ctg	aag	tat	gag	gtg	480
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val	
145				150						155				160		
gca	ttc	tgg	aag	gag	ggg	gcc	gga	aac	aag	gtg	gga	agc	tcc	ttt	cct	528
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Val	Gly	Ser	Ser	Phe	Pro	
				165				170						175		
gcc	ccc	agg	cta	ggc	ccg	ctc	ctc	cac	ccc	ttc	tta	ctc	agg	ttc	ttc	576
Ala	Pro	Arg	Leu	Gly	Pro	Leu	Leu	His	Pro	Phe	Leu	Leu	Arg	Phe	Phe	
		180						185				190				
tca	ccc	tcc	cag	cct	gct	cct	gca	ccc	ctc	ctc	cag	gaa	gtc	ttc	cct	624
Ser	Pro	Ser	Gln	Pro	Ala	Pro	Ala	Pro	Leu	Leu	Gln	Glu	Val	Phe	Pro	
		195				200						205				
gta	cac	tcc	tgacttctg	cagtcagccc	taataaaaatc	tgatcaaagt										673
Val	His	Ser														
210																

674

[illegible]

<210> 22
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>

<223> Zcytor17-Fc4 fusion protein

<221> CDS

<222> (1)...(1422)

<400> 22

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Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Val	Leu	Leu	Leu	Cys	Gly	
1				5				10						15		

gcc	gtc	ttc	gtt	tcg	ctc	agc	cag	gaa	atc	cat	gcc	gag	ttg	aga	cgc	96
Ala	Val	Phe	Val	Ser	Leu	Ser	Gln	Glu	Ile	His	Ala	Glu	Leu	Arg	Arg	
			20					25					30			

ttc	cgt	aga	tcc	agg	ccc	cgt	ctg	gcc	cct	ccc	cag	aat	gtg	acg	ctg	144
Phe	Arg	Arg	Ser	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu	
			35				40					45				

ctc	tcc	cag	aac	ttc	agc	gtg	tac	ctg	aca	tgg	ctc	cca	ggg	ctt	ggc	192
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly	
	50					55				60						

aac	ccc	cag	gat	gtg	acc	tat	ttt	gtg	gcc	tat	cag	agc	tct	ccc	acc	240
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr	
65					70				75					80		

cgt	aga	cgg	tgg	cgc	gaa	gtg	gaa	gag	tgt	gcg	gga	acc	aag	gag	ctg	288
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu	
				85				90						95		

cta	tgt	tct	atg	atg	tgc	ctg	aag	aaa	cag	gac	ctg	tac	aac	aag	ttc	336
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe	
			100				105					110				

aag	gga	cgc	gtg	cgg	acg	gtt	tct	ccc	agc	tcc	aag	tcc	ccc	tgg	gtg	384
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val	
	115					120					125					

gag	tcc	gaa	tac	ctg	gat	tac	ctt	ttt	gaa	gtg	gag	ccg	gcc	cca	cct	432
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro	
130						135				140						

gtc	ctg	gtg	ctc	acc	cag	acg	gag	gag	atc	ctg	agt	gcc	aat	gcc	acg	480
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr	
145					150					155					160	
tac	cag	ctg	ccc	ccc	tgc	atg	ccc	cca	ctg	gat	ctg	aag	tat	gag	gtg	528
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val	
				165					170					175		
gca	ttc	tgg	aag	gag	ggg	gcc	gga	aac	aag	acc	cta	ttt	cca	gtc	act	576
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr	
			180					185					190			
ccc	cat	ggc	cag	cca	gtc	cag	atc	act	ctc	cag	cca	gct	gcc	agc	gaa	624
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu	
		195					200					205				
cac	cac	tgc	ctc	agt	gcc	aga	acc	atc	tac	acg	ttc	agt	gtc	ccg	aaa	672
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys	
	210					215					220					
tac	agc	aag	ttc	tct	aag	ccc	acc	tgc	ttc	ttg	ctg	gag	gtc	cca	gaa	720
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu	
225					230					235					240	
gcc	aac	tgg	aga	tct	tca	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	768
Ala	Asn	Trp	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	
				245					250					255		
gca	cct	gaa	gcc	gag	ggg	gca	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	816
Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	
			260					265					270			
ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	864
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	
		275					280					285				
gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	912
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	
	290					295					300					
gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	960
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	
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cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac 1008
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 325 330 335

cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa 1056
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 340 345 350

gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc aaa ggg cag 1104
 Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 355 360 365

ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg 1152
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 370 375 380

acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc 1200
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 385 390 395 400

agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac 1248
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 405 410 415

tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc 1296
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 420 425 430

tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc 1344
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 435 440 445

ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag 1392
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
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<211> 473

<212> PRT

<213> Artificial Sequence

<400> 23

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			20					25					30		
Phe	Arg	Arg	Ser	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu
			35				40					45			
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly
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Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr
65					70					75				80	
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu
				85					90					95	
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe
			100					105					110		
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val
	115					120						125			
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro
	130					135					140				
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr
145					150					155				160	
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val
				165					170					175	
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr
			180					185					190		
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu
	195					200					205				
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys
	210					215					220				
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu
225					230					235				240	
Ala	Asn	Trp	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
				245					250					255	
Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
	260						265						270		
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
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	290					295						300			

00995555 1122004

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 305 310 315 320
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 325 330 335
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 340 345 350
 Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 355 360 365
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 370 375 380
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 385 390 395 400
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 405 410 415
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 420 425 430
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 435 440 445
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
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<210> 24

<211> 28

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<213> Artificial Sequence

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<210> 26

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<400> 26

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<210> 27

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<223> Oligonucleotide primer ZC37681

<400> 27

cctcgctcc tcttctctct ca

22

<210> 28

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

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NO:19

<221> misc_feature

<222> (1)...(1560)

<223> n = A,T,C or G

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mgncnmgny tngcncncc ncaraaygt acnytnytnw sncaraaytt ywsngntay	120
ytnacntggy tncnggnyt nggnaayccn cargaygt naaytttgt ngcntaycar	180
wsnwsnccna cnmgmgnmg ntggmngar gtngargart gygcnggnac naargarytn	240
ytntgywsna tgatgtggyt naaraarcar gayytnaya ayaarttyaa rggnmgngtn	300

mgnacngtnw	sncnwsnws	naarwsnccn	tgggtngarw	sngartayyt	ngaytayytn	360
ttygargtn	arcngcncc	nccngtnytn	gtnytnacnc	aracngarga	rathytnwsn	420
gcnaaygcna	cntaycaryt	nccncntgy	atgccnccny	tngayytnaa	rtaygargtn	480
gcnttytgga	argarggngc	nggnaayaar	acnytnntyc	cngtnacncc	ncayggncar	540
ccngtncara	thacnytnca	rccngcngcn	wsngarcayc	aytggytnws	ngcnmgnacn	600
athtayacnt	tywsngtncc	naartaywsn	aarttywsna	arccnacntg	ytttytnytn	660
gargtnccng	argcnaaytg	ggcnttyytn	gtnytnccnw	snytnytnat	hytnytnytn	720
gtnathgcng	cngggnggt	nathtggaar	acnytnatgg	gnaayccntg	gttycarmgn	780
gcnaaratgc	cnmgngcny	ngayttywsn	ggncayacnc	ayccngtngc	nacnttycar	840
ccnwsnmgnc	cngarwsngt	naaygayytn	ttyytnngyc	cncaraarga	rytnacnmgn	900
ggngtnmgnc	cnacnccnmg	ngtnmgngcn	ccngcnacnc	arcaracnmg	ntggaaraar	960
gayytnngcng	argaygarga	rgargargay	gargargaya	cngargaygg	ngtnwsntty	1020
carcentaya	thgarccncc	nwsnttyytn	ggncargarc	aycargcncc	nggncaywsn	1080
gargcnggng	ngtngayws	nggnmgncn	mgngcnccny	tngtnccnws	ngarggnwsn	1140
wsngcntggg	aywsnwsnga	ymgnwsntgg	gcnwsnacng	tngaywsnws	ntgggaymgn	1200
gcnggnwsnw	snggntayyt	ngcngaraar	ggncnccngc	arggncnccg	nggngaygg	1260
caycargarw	snytnccncc	nccngartty	wsnaargayw	snggnttyyt	ngargarytn	1320
ccngargaya	ayytnwsnws	ntgggcnacn	tggggnacny	tnccnccnga	rccnaayytn	1380
gtncnccngg	gncnccnct	nwsnytnear	acnytnacnt	tytgytgga	rwsnwsnccn	1440
gargargarg	argargcnmg	ngarwsngar	athgargayw	sngaygcngg	nwsntggggg	1500
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<210> 29

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

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<221> misc_feature

<222> (1)...(633)

<223> n = A,T,C or G

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ytnacntggy	tnccnccngy	nggnaayccn	cargaygt	na	ntaytygt	180
wsnwsnccna	cnmgngmng	ntggmgngar	gtngargart	gygcnggnac	naargarytn	240
ytnytnytnw	tgatgtgyt	naaraarcar	gayytnytna	ayaarttyaa	rggnmgngtn	300
mgnacngtnw	sncnwsnws	naarwsnccn	tgggtngarw	sngartayyt	ngaytayytn	360
ttygargtn	arcngcncc	nccngtnytn	gtnytnacnc	aracngarga	rathytnwsn	420
gcnaaygcna	cntaycaryt	nccncntgy	atgccnccny	tngayytnaa	rtaygargtn	480

gcnttytgga argarggngc nggnaayaar gtnggnwsnw snattyccngc nccnmgnytn 540
 ggncenytny tncayccntt yytnytnmgn ttyttywsnc cnwsncarcc ngcncngcn 600
 ccnytnytn c argargtntt yccngtncay wsn 633

<210> 30

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Primer ZC39204

<400> 30

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 ccag 64

<210> 31

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Primer ZC39205

<400> 31

tctgtatcag gctgaaaatc ttatctcatc cgccaaaaca ccagttggct tctgggacct 60
 ccag 64

<210> 32

<211> 1922

<212> DNA

<213> Artificial Sequence

<220>

<223> MBP-human zcytoR19 fusion protein polynucleotide
 sequence

<221> CDS

<222> (123)...(1922)

<400> 32

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 caggaaacag ccagtcctgt taggtgtttt cagcagcact tcaccaacaa ggaccataga 120

tt atg aaa act gaa gaa ggt aaa ctg gta atc tgg att aac ggc gat	167
Met Lys Thr Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp	
1 5 10 15	
aaa ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat	215
Lys Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp	
20 25 30	
acc gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa	263
Thr Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys	
35 40 45	
ttc cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg	311
Phe Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp	
50 55 60	
gca cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa	359
Ala His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu	
65 70 75	
atc acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg	407
Ile Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp	
80 85 90 95	
gat gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt	455
Asp Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val	
100 105 110	
gaa gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca	503
Glu Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro	
115 120 125	
aaa acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa	551
Lys Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys	
130 135 140	
ggt aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg	599
Gly Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp	
145 150 155	
ccg ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc	647
Pro Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly	
160 165 170 175	

aag tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg	695
Lys Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala	
180 185 190	
ggt ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca	743
Gly Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala	
195 200 205	
gac acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca	791
Asp Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr	
210 215 220	
gcg atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc	839
Ala Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser	
225 230 235	
aaa gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca	887
Lys Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro	
240 245 250 255	
tcc aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt	935
Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser	
260 265 270	
ccg aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act	983
Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr	
275 280 285	
gat gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta	1031
Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val	
290 295 300	
gcg ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc	1079
Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala	
305 310 315	
gcc acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg	1127
Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro	
320 325 330 335	
cag atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc	1175

Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala	
340 345 350	
gcc agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act	1223
Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr	
355 360 365	
aat tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg	1271
Asn Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu	
370 375 380	
gtt ccg cgt gga tcc agg ccc cgt ctg gcc cct ccc cag aat gtg acg	1319
Val Pro Arg Gly Ser Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr	
385 390 395	
ctg ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt	1367
Leu Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu	
400 405 410 415	
ggc aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc	1415
Gly Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro	
420 425 430	
acc cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag	1463
Thr Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu	
435 440 445	
ctg cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag	1511
Leu Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys	
450 455 460	
ttc aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg	1559
Phe Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp	
465 470 475	
gtg gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca	1607
Val Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro	
480 485 490 495	
cct gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc	1655
Pro Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala	
500 505 510	

acg tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag 1703
 Thr Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu
 515 520 525

gtg gca ttc tgg aag gag ggg gcc gga aac aag acc cta ttt cca gtc 1751
 Val Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val
 530 535 540

act ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc 1799
 Thr Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser
 545 550 555

gaa cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg 1847
 Glu His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro
 560 565 570 575

aaa tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca 1895
 Lys Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro
 580 585 590

gaa gcc aac tgg tgt ttt ggc gga tga 1922
 Glu Ala Asn Trp Cys Phe Gly Gly *
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<210> 33

<211> 599

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP-human zcytoR19 fusion protein polypeptide
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<400> 33

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 20 25 30
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
 35 40 45
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 50 55 60

His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
 65 70 75 80
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
 85 90 95
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
 100 105 110
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
 115 120 125
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
 130 135 140
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160
 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
 165 170 175
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
 180 185 190
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365
 Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val
 370 375 380
 Pro Arg Gly Ser Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 385 390 395 400

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<210> 34
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<213> Homo sapiens

<220>
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<222> (1)...(20)
<223> Xaa = Any Amino Acid
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Asn Phe Ser Val
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<210> 35
 <211> 24
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC40285

<400> 35
 gccccagcca cccaacagac aaga 24

<210> 36
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC40286

<400> 36
 ccaggtggcc caggaggaga gggt 24

<210> 37
 <211> 24
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC39128

<400> 37
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<210> 38
 <211> 24
 <212> DNA
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<220>
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<400> 38
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<210> 39
 <211> 25
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<220>
 <223> Oligonucleotide primer ZC40784

<400> 39
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<210> 40
 <211> 25
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC40785

<400> 40
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<210> 41
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 <223> Oligonucleotide primer ZC40786

<400> 41
 gggaattcct gcagaaactc agta 24

<210> 42
 <211> 24
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC40787

<400> 42

cccttcctgc tcctttgact gcgt

24

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39408

<400> 43

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25

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<223> forward zcytor19 knockout oligonucleotide

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21